

## **RAW SEQUENCE LISTING**

**The Biotechnology Systems Branch of the Scientific and Technical  
Information Center (STIC) no errors detected.**

Application Serial Number: 10/521,693  
Source: Pg  
Date Processed by STIC: 1/26/06

# ***ENTERED***



PCT

## RAW SEQUENCE LISTING

DATE: 01/26/2006

PATENT APPLICATION: US/10/521,693

TIME: 08:48:06

Input Set : F:\10.521693 seq 1st.txt

Output Set: N:\CRF4\01262006\J521693.raw

3 <110> APPLICANT: AKZO Nobel N.V.  
 5 <120> TITLE OF INVENTION: novel Brachyspira hyodysenteriae vaccine  
 7 <130> FILE REFERENCE: Bhyovaccine  
 C--> 9 <140> CURRENT APPLICATION NUMBER: US/10/521,693  
 C--> 9 <141> CURRENT FILING DATE: 2005-01-18  
 9 <160> NUMBER OF SEQ ID NOS: 4  
 11 <170> SOFTWARE: PatentIn version 3.1  
 13 <210> SEQ ID NO: 1  
 14 <211> LENGTH: 1614  
 15 <212> TYPE: DNA  
 16 <213> ORGANISM: Brachyspira hyodysenteria  
 18 <220> FEATURE:  
 19 <221> NAME/KEY: CDS  
 20 <222> LOCATION: (1)..(1611)  
 21 <223> OTHER INFORMATION:  
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 26 Met Lys Lys Leu Tyr Ser Leu Phe Ile Phe Ile Ala Val Ile Leu Phe  
 27 1 5 10 15  
 29 att tat tca tgc gga agt tat ttt aat cct aaa tac tat ttt ttt aaa 96  
 30 Ile Tyr Ser Cys Gly Ser Tyr Phe Asn Pro Lys Tyr Tyr Phe Phe Lys  
 31 20 25 30  
 33 agt aaa gta gag aat aat gga agt tct gga agc tca ggc ggt aat tca 144  
 34 Ser Lys Val Glu Asn Asn Gly Ser Ser Gly Ser Ser Gly Gly Asn Ser  
 35 35 40 45  
 37 gga ata tat ata cag cct ggt gaa gat gaa gat cct ttt aca gca cct 192  
 38 Gly Ile Tyr Ile Gln Pro Gly Glu Asp Glu Asp Pro Phe Thr Ala Pro  
 39 50 55 60  
 41 aaa tat gca tct gag tgg tgg aat gat cct aat aat ggt gga ttt gat 240  
 42 Lys Tyr Ala Ser Glu Trp Trp Asn Asp Pro Asn Asn Gly Gly Phe Asp  
 43 65 70 75 80  
 45 gct tcg gat ata gat aaa tgg ttt ttg aaa gtt gaa ttt tta gca aat 288  
 46 Ala Ser Asp Ile Asp Lys Trp Phe Leu Lys Val Glu Phe Leu Ala Asn  
 47 85 90 95  
 49 gat tat cca agt tac aga ttt tta aca aaa agc gga aga aaa gca gga 336  
 50 Asp Tyr Pro Ser Tyr Arg Phe Leu Thr Lys Ser Gly Arg Lys Ala Gly  
 51 100 105 110  
 53 cat gtt tgg gta gtt tct aat gaa caa tct cag gca tat tta gat caa 384  
 54 His Val Trp Val Val Ser Asn Glu Gln Ser Gln Ala Tyr Leu Asp Gln  
 55 115 120 125  
 57 gga gaa gta tgc aat act aca gca gtt acc ggg gta tct ata aaa cca 432  
 58 Gly Glu Val Cys Asn Thr Thr Ala Val Thr Gly Val Ser Ile Lys Pro  
 59 130 135 140

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61 gta gca aat gta aca gga gta aca tat aca aaa tat aag gga ttg aat      480
62 Val Ala Asn Val Thr Gly Val Thr Tyr Thr Lys Tyr Lys Gly Leu Asn
63 145                               150                               155                               160
65 gca aga ttt ttc act cat gac gga gat tat cat aat gta tat cct gga      528
66 Ala Arg Phe Phe Thr His Asp Gly Asp Tyr His Asn Val Tyr Pro Gly
67                               165                               170                               175
69 aaa gat aag ata agc aga ttc tat ttt tat tat ttt aca ggt act ccg      576
70 Lys Asp Lys Ile Ser Arg Phe Tyr Phe Tyr Tyr Phe Thr Gly Thr Pro
71                               180                               185                               190
73 gaa atg gct aaa ttt tta gaa aat tgc tta ata gct gta gac aca tac      624
74 Glu Met Ala Lys Phe Leu Glu Asn Cys Leu Ile Ala Val Asp Thr Tyr
75                               195                               200                               205
77 tca aaa cta tta ttt tac tat gga aga cct caa agc gat tat cca aat      672
78 Ser Lys Leu Leu Phe Tyr Tyr Gly Arg Pro Gln Ser Asp Tyr Pro Asn
79                               210                               215                               220
81 cct cca agc tgg cag aag cct agt aat ttg gtt gat aaa tac tct cct      720
82 Pro Pro Ser Trp Gln Lys Pro Ser Asn Leu Val Asp Lys Tyr Ser Pro
83 225                               230                               235                               240
85 aca ggt tat tgg ata tct ata gat gaa ggt ata aat gat aag ggg cag      768
86 Thr Gly Tyr Trp Ile Ser Ile Asp Glu Gly Ile Asn Asp Lys Gly Gln
87                               245                               250                               255
89 aat tat cct ttt tat gaa tat gat cct gta gga tat gta aaa agc gat      816
90 Asn Tyr Pro Phe Tyr Glu Tyr Asp Pro Val Gly Tyr Val Lys Ser Asp
91                               260                               265                               270
93 ggt aca gtt gtt ata ttt gat tgg ttt gca aac aga tta aga gga aat      864
94 Gly Thr Val Val Ile Phe Asp Trp Phe Ala Asn Arg Leu Arg Gly Asn
95                               275                               280                               285
97 cat aat aat gat cct ata aaa agt gat cct aaa gga gct att gtt cct      912
98 His Asn Asn Asp Pro Ile Lys Ser Asp Pro Lys Gly Ala Ile Val Pro
99                               290                               295                               300
101 aat cct aat act aat cct tct gct tca act aca gga cgt tct cct tat      960
102 Asn Pro Asn Thr Asn Pro Ser Ala Ser Thr Thr Gly Arg Ser Pro Tyr
103 305                               310                               315                               320
105 gca ttc tat tcg cct tta gca caa aaa gat aaa act aaa ata act ata      1008
106 Ala Phe Tyr Ser Pro Leu Ala Gln Lys Asp Lys Thr Lys Ile Thr Ile
107                               325                               330                               335
109 agt act aca aaa tta ata aat tat aca gtt ttc agt tat aaa tac agt      1056
110 Ser Thr Thr Lys Leu Ile Asn Tyr Thr Val Phe Ser Tyr Lys Tyr Ser
111                               340                               345                               350
113 ata caa ata ttt ccg cct agt atg aaa gaa gaa aaa ctt cct tat gct      1104
114 Ile Gln Ile Phe Pro Pro Ser Met Lys Glu Glu Lys Leu Pro Tyr Ala
115                               355                               360                               365
117 tat att gca tat gct tcc tat ggt gca gct tat caa aat gaa agc agc      1152
118 Tyr Ile Ala Tyr Ala Ser Tyr Gly Ala Ala Tyr Gln Asn Glu Ser Ser
119                               370                               375                               380
121 aaa tct gta gag atg ata tct gat ata aat aaa gga gag cat tac gga      1200
122 Lys Ser Val Glu Met Ile Ser Asp Ile Asn Lys Gly Glu His Tyr Gly
123 385                               390                               395                               400
125 agt att aca aga ata agc act gta cct aaa ata gat aaa gac gga gga      1248

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126 Ser Ile Thr Arg Ile Ser Thr Val Pro Lys Ile Asp Lys Asp Gly Gly
127          405          410          415
129 gag ttg gta aaa gaa gga tct aag tct ttt gaa tta tat ggt att gat      1296
130 Glu Leu Val Lys Glu Gly Ser Lys Ser Phe Glu Leu Tyr Gly Ile Asp
131          420          425          430
133 act aaa gat aca ttt ata gaa tta agt tta aaa cta att aaa aat gat      1344
134 Thr Lys Asp Thr Phe Ile Glu Leu Ser Leu Lys Leu Ile Lys Asn Asp
135          435          440          445
137 gaa aat aca gaa ttt gtt gat caa gga aca gca ggt act ggt cct tta      1392
138 Glu Asn Thr Glu Phe Val Asp Gln Gly Thr Ala Gly Thr Gly Pro Leu
139          450          455          460
141 gta tac ttt gat aaa aca gat cct ata ctt gta tta aaa tat gat aaa      1440
142 Val Tyr Phe Asp Lys Thr Asp Pro Ile Leu Val Leu Lys Tyr Asp Lys
143 465          470          475          480
145 tct tct gac agc ttc aaa tac agc agt gta aaa gga aac aag caa ata      1488
146 Ser Ser Asp Ser Phe Lys Tyr Ser Ser Val Lys Gly Asn Lys Gln Ile
147          485          490          495
149 gaa gtt gac agc aat tta tca att aaa aga gga gag aat aaa gag ttt      1536
150 Glu Val Asp Ser Asn Leu Ser Ile Lys Arg Gly Glu Asn Lys Glu Phe
151          500          505          510
153 aca gtt aaa ttt aaa gat cca aat aat gga aat gag ttt ggg gtt gta      1584
154 Thr Val Lys Phe Lys Asp Pro Asn Asn Gly Asn Glu Phe Gly Val Val
155          515          520          525
157 ttt aaa ata gat ttt gaa aaa ata tca tga      1614
158 Phe Lys Ile Asp Phe Glu Lys Ile Ser
159          530          535
162 <210> SEQ ID NO: 2
163 <211> LENGTH: 537
164 <212> TYPE: PRT
165 <213> ORGANISM: Brachyspira hyodysenteria
167 <400> SEQUENCE: 2
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170 1          5          10          15
173 Ile Tyr Ser Cys Gly Ser Tyr Phe Asn Pro Lys Tyr Tyr Phe Phe Lys
174          20          25          30
177 Ser Lys Val Glu Asn Asn Gly Ser Ser Gly Ser Ser Gly Asn Ser
178          35          40          45
181 Gly Ile Tyr Ile Gln Pro Gly Glu Asp Glu Asp Pro Phe Thr Ala Pro
182          50          55          60
185 Lys Tyr Ala Ser Glu Trp Trp Asn Asp Pro Asn Asn Gly Gly Phe Asp
186 65          70          75          80
189 Ala Ser Asp Ile Asp Lys Trp Phe Leu Lys Val Glu Phe Leu Ala Asn
190          85          90          95
193 Asp Tyr Pro Ser Tyr Arg Phe Leu Thr Lys Ser Gly Arg Lys Ala Gly
194          100          105          110
197 His Val Trp Val Val Ser Asn Glu Gln Ser Gln Ala Tyr Leu Asp Gln
198          115          120          125
201 Gly Glu Val Cys Asn Thr Thr Ala Val Thr Gly Val Ser Ile Lys Pro
202          130          135          140

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205 Val Ala Asn Val Thr Gly Val Thr Tyr Thr Lys Tyr Lys Gly Leu Asn
206 145 150 155 160
209 Ala Arg Phe Phe Thr His Asp Gly Asp Tyr His Asn Val Tyr Pro Gly
210 165 170 175
213 Lys Asp Lys Ile Ser Arg Phe Tyr Phe Tyr Tyr Phe Thr Gly Thr Pro
214 180 185 190
217 Glu Met Ala Lys Phe Leu Glu Asn Cys Leu Ile Ala Val Asp Thr Tyr
218 195 200 205
221 Ser Lys Leu Leu Phe Tyr Tyr Gly Arg Pro Gln Ser Asp Tyr Pro Asn
222 210 215 220
225 Pro Pro Ser Trp Gln Lys Pro Ser Asn Leu Val Asp Lys Tyr Ser Pro
226 225 230 235 240
229 Thr Gly Tyr Trp Ile Ser Ile Asp Glu Gly Ile Asn Asp Lys Gly Gln
230 245 250 255
233 Asn Tyr Pro Phe Tyr Glu Tyr Asp Pro Val Gly Tyr Val Lys Ser Asp
234 260 265 270
237 Gly Thr Val Val Ile Phe Asp Trp Phe Ala Asn Arg Leu Arg Gly Asn
238 275 280 285
241 His Asn Asn Asp Pro Ile Lys Ser Asp Pro Lys Gly Ala Ile Val Pro
242 290 295 300
245 Asn Pro Asn Thr Asn Pro Ser Ala Ser Thr Thr Gly Arg Ser Pro Tyr
246 305 310 315 320
249 Ala Phe Tyr Ser Pro Leu Ala Gln Lys Asp Lys Thr Lys Ile Thr Ile
250 325 330 335
253 Ser Thr Thr Lys Leu Ile Asn Tyr Thr Val Phe Ser Tyr Lys Tyr Ser
254 340 345 350
257 Ile Gln Ile Phe Pro Pro Ser Met Lys Glu Glu Lys Leu Pro Tyr Ala
258 355 360 365
261 Tyr Ile Ala Tyr Ala Ser Tyr Gly Ala Ala Tyr Gln Asn Glu Ser Ser
262 370 375 380
265 Lys Ser Val Glu Met Ile Ser Asp Ile Asn Lys Gly Glu His Tyr Gly
266 385 390 395 400
269 Ser Ile Thr Arg Ile Ser Thr Val Pro Lys Ile Asp Lys Asp Gly Gly
270 405 410 415
273 Glu Leu Val Lys Glu Gly Ser Lys Ser Phe Glu Leu Tyr Gly Ile Asp
274 420 425 430
277 Thr Lys Asp Thr Phe Ile Glu Leu Ser Leu Lys Leu Ile Lys Asn Asp
278 435 440 445
281 Glu Asn Thr Glu Phe Val Asp Gln Gly Thr Ala Gly Thr Gly Pro Leu
282 450 455 460
285 Val Tyr Phe Asp Lys Thr Asp Pro Ile Leu Val Leu Lys Tyr Asp Lys
286 465 470 475 480
289 Ser Ser Asp Ser Phe Lys Tyr Ser Ser Val Lys Gly Asn Lys Gln Ile
290 485 490 495
293 Glu Val Asp Ser Asn Leu Ser Ile Lys Arg Gly Glu Asn Lys Glu Phe
294 500 505 510
297 Thr Val Lys Phe Lys Asp Pro Asn Asn Gly Asn Glu Phe Gly Val Val
298 515 520 525
301 Phe Lys Ile Asp Phe Glu Lys Ile Ser

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305 <210> SEQ ID NO: 3
306 <211> LENGTH: 540
307 <212> TYPE: DNA
308 <213> ORGANISM: Brachyspira hyodysenteria
310 <220> FEATURE:
311 <221> NAME/KEY: CDS
312 <222> LOCATION: (1)..(537)
313 <223> OTHER INFORMATION:
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319 1      5      10      15
321 gga tgt gaa act atg cag cct aaa aat aat gat aca att gta aaa aat      96
322 Gly Cys Glu Thr Met Gln Pro Lys Asn Asn Asp Thr Ile Val Lys Asn
323      20      25      30
325 gat aat tca tct aat gaa gat aaa aaa gaa gaa act ata act aga gaa      144
326 Asp Asn Ser Ser Asn Glu Asp Lys Lys Glu Glu Thr Ile Thr Arg Glu
327      35      40      45
329 gat aca cca aaa atg aaa gtt aca gtt tat gga gca gat aaa gaa att      192
330 Asp Thr Pro Lys Met Lys Val Thr Val Tyr Gly Ala Asp Lys Glu Ile
331      50      55      60
333 caa gct gtg gaa ata aat gat aaa act tat tat gta ata ggc gga aaa      240
334 Gln Ala Val Glu Ile Asn Asp Lys Thr Tyr Tyr Val Ile Gly Gly Lys
335 65      70      75      80
337 gat gtt gag aat atg aca gaa gct gat ata aaa aaa tca tct tta gta      288
338 Asp Val Glu Asn Met Thr Glu Ala Asp Ile Lys Lys Ser Ser Leu Val
339      85      90      95
341 gca cct tta aaa gtt aca gaa gaa act gtt aat ggt aca aga ggt ata      336
342 Ala Pro Leu Lys Val Thr Glu Glu Thr Val Asn Gly Thr Arg Gly Ile
343      100      105      110
345 gtt gtt aca tat tat gat gta aaa gta ttc ttg ggt aaa aga aca gga      384
346 Val Val Thr Tyr Tyr Asp Val Lys Val Phe Leu Gly Lys Arg Thr Gly
347      115      120      125
349 aca gga act atc gta gga ata ttc gag cct cag aaa aat gat tgg act      432
350 Thr Gly Thr Ile Val Gly Ile Phe Glu Pro Gln Lys Asn Asp Trp Thr
351      130      135      140
353 aca gga aat gat ttg gat aga agt tta tct att caa ata aaa tta tct      480
354 Thr Gly Asn Asp Leu Asp Arg Ser Leu Ser Ile Gln Ile Lys Leu Ser
355 145      150      155      160
357 aga aat ata gca ggt cct ata gat ata aaa aga gga agc ata tct tta      528
358 Arg Asn Ile Ala Gly Pro Ile Asp Ile Lys Arg Gly Ser Ile Ser Leu
359      165      170      175
361 gca ttt aat taa      540
362 Ala Phe Asn
366 <210> SEQ ID NO: 4
367 <211> LENGTH: 179
368 <212> TYPE: PRT
369 <213> ORGANISM: Brachyspira hyodysenteria

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VERIFICATION SUMMARY

PATENT APPLICATION: US/10/521,693

DATE: 01/26/2006

TIME: 08:48:07

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Output Set: N:\CRF4\01262006\J521693.raw

L:9 M:270 C: Current Application Number differs, Replaced Current Application No

L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:24 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:21

L:316 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:3,Line#:313